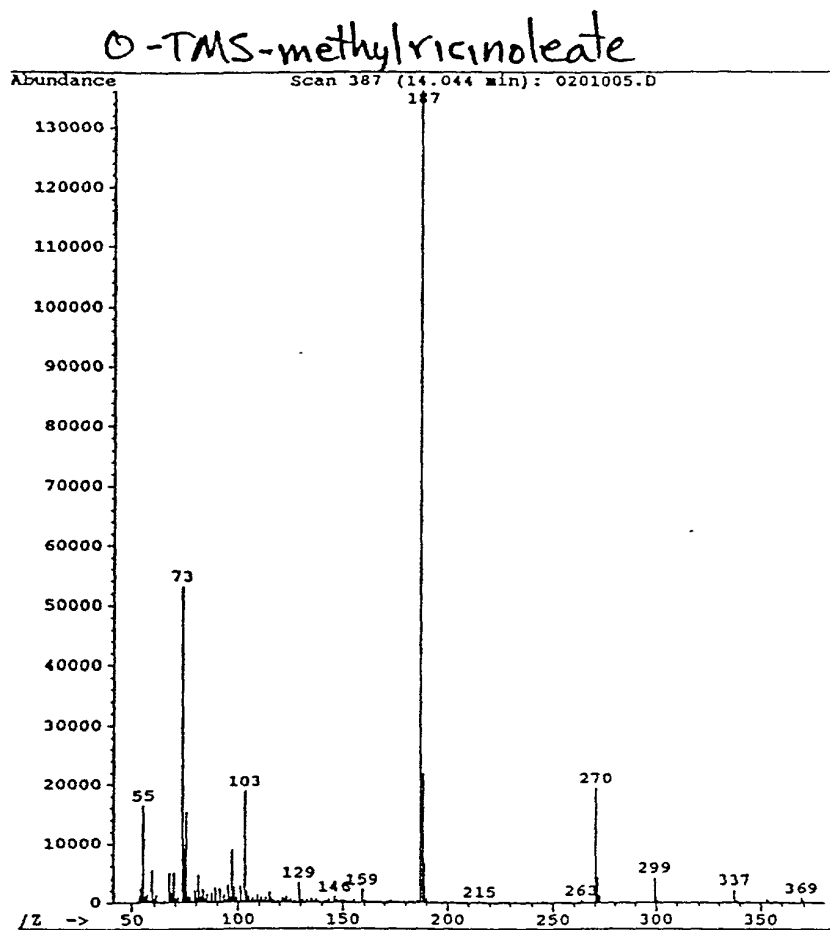
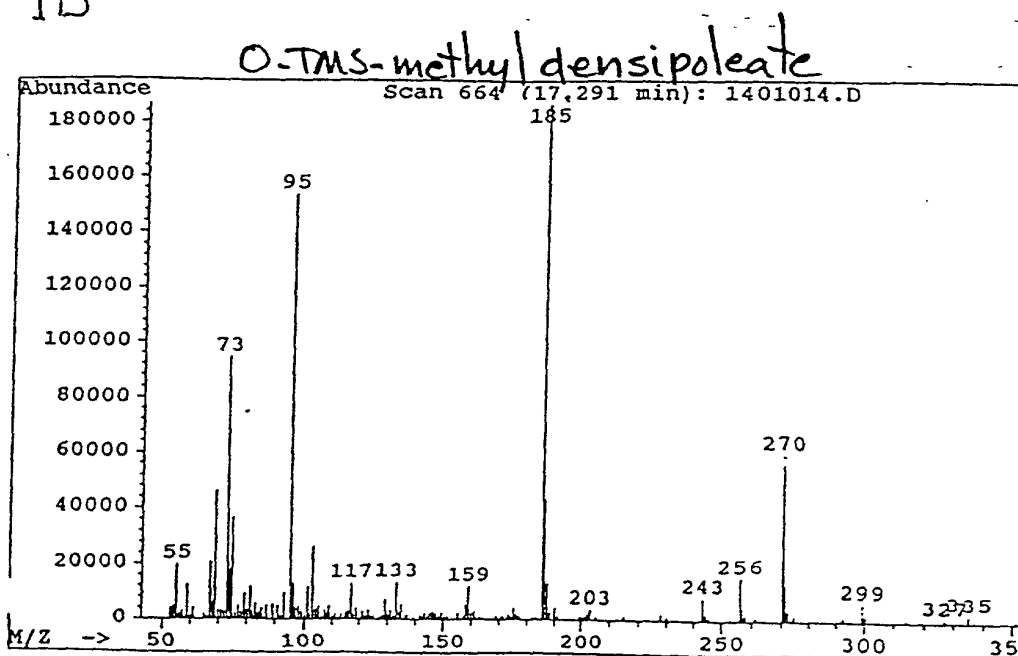


Figure

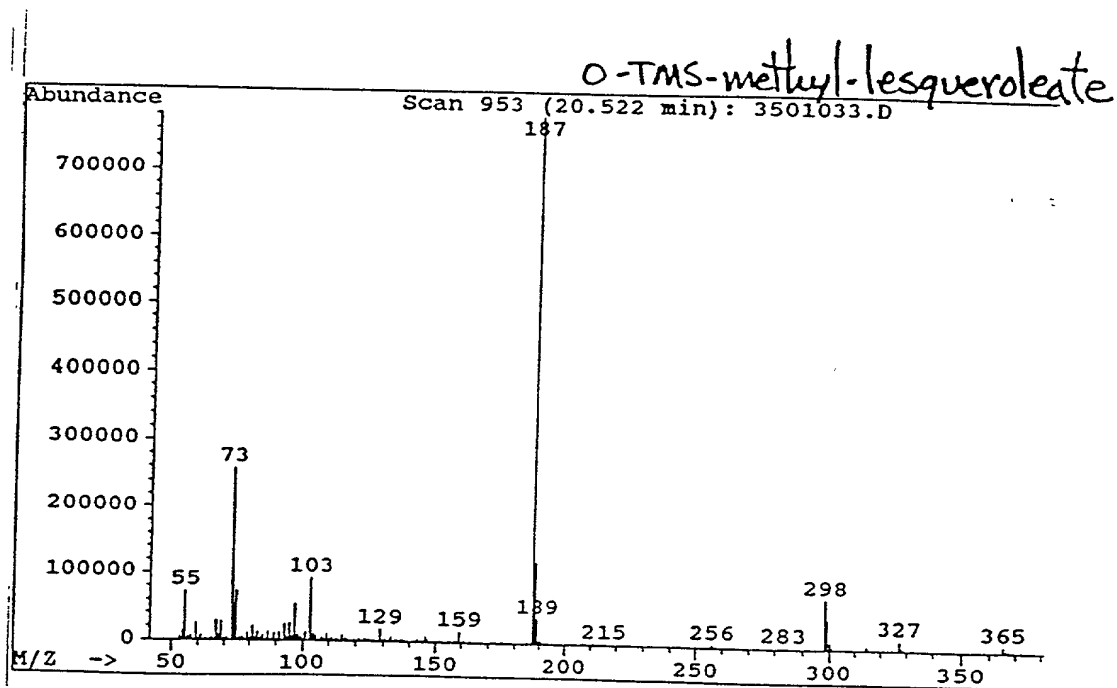
1A



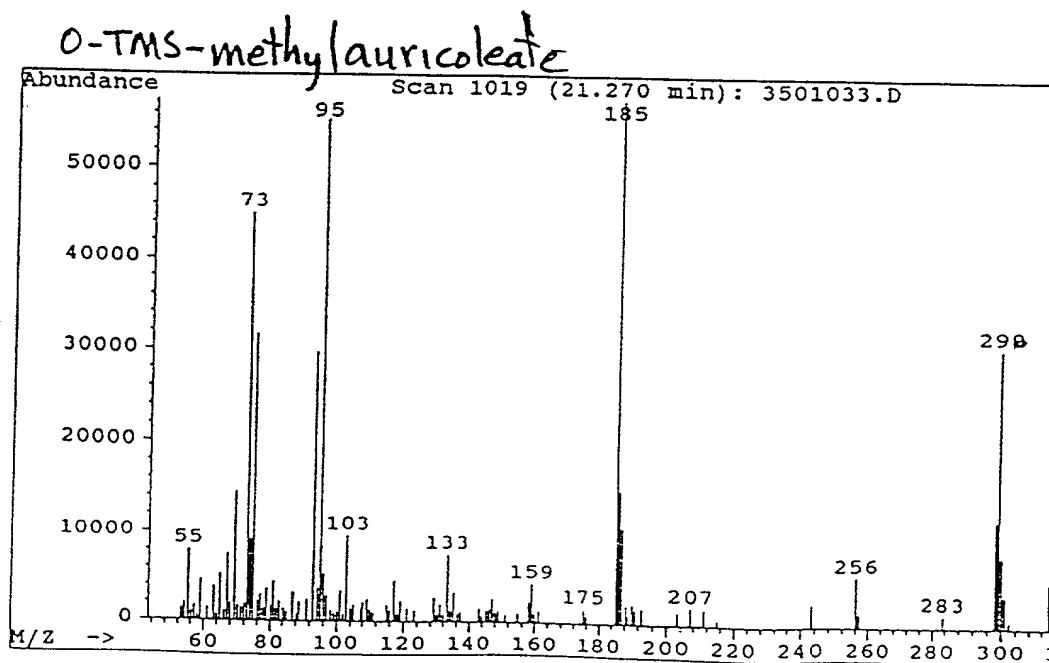
1B



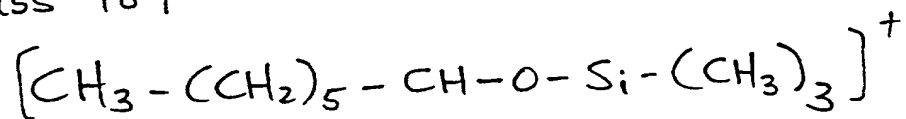
1C



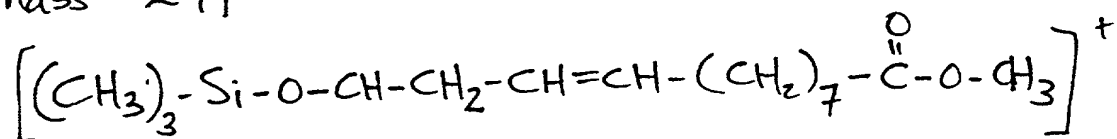
1D



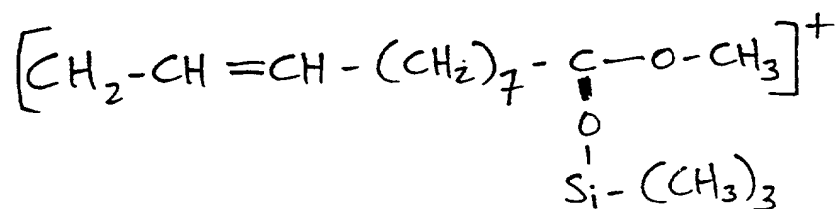
Ion #1: Mass 187



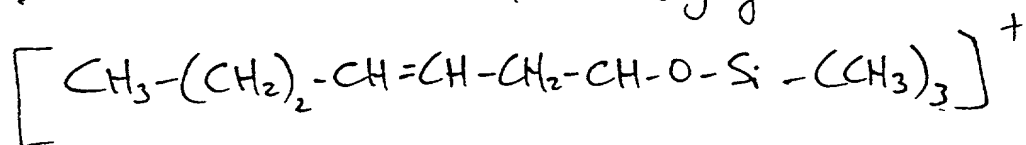
Ion #2: Mass 299



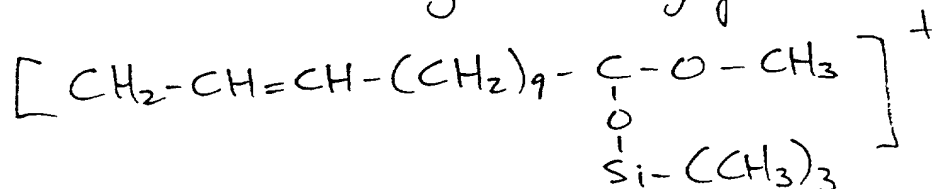
Ion #3: Mass 270 (characteristic rearrangement ion)



Ion #4: Mass 185 (desaturated analog of Ion #1)



Ion #5: Mass 298 (elongated analog of Ion #3)



Ion #6: Mass 327 (elongated analog of Ion #2)

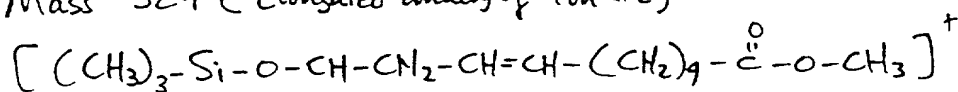


Figure 2.

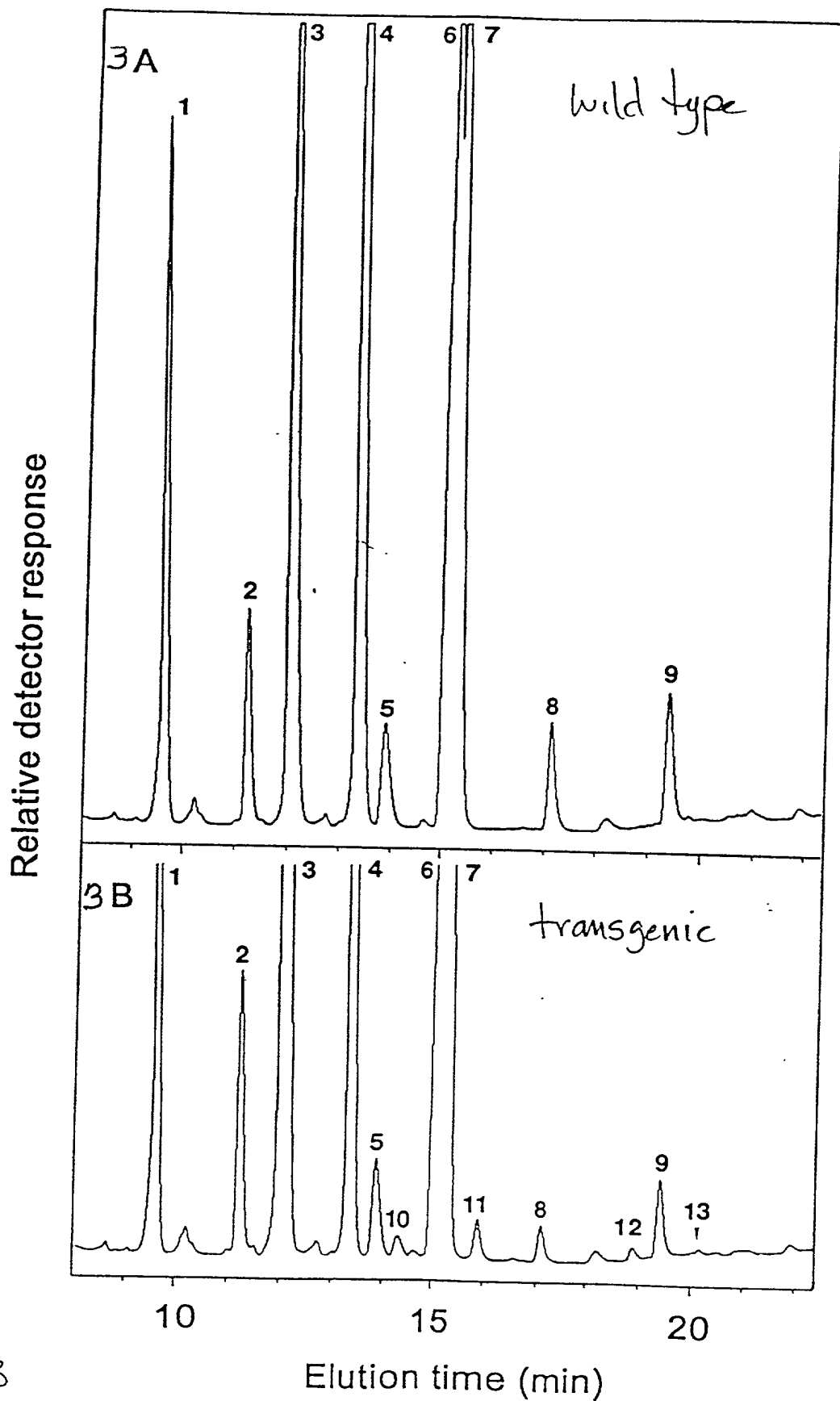
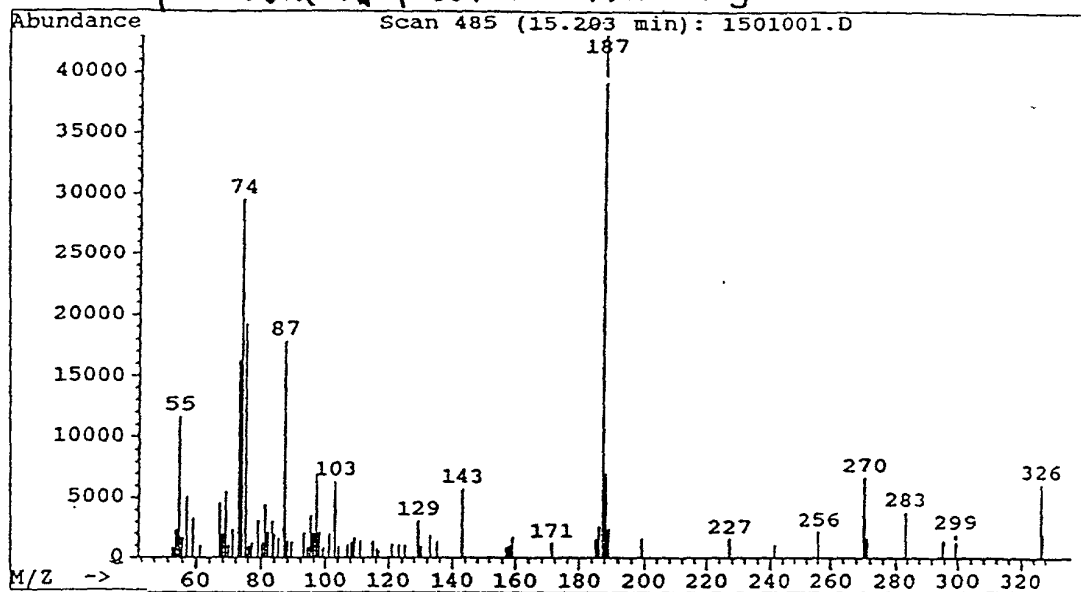


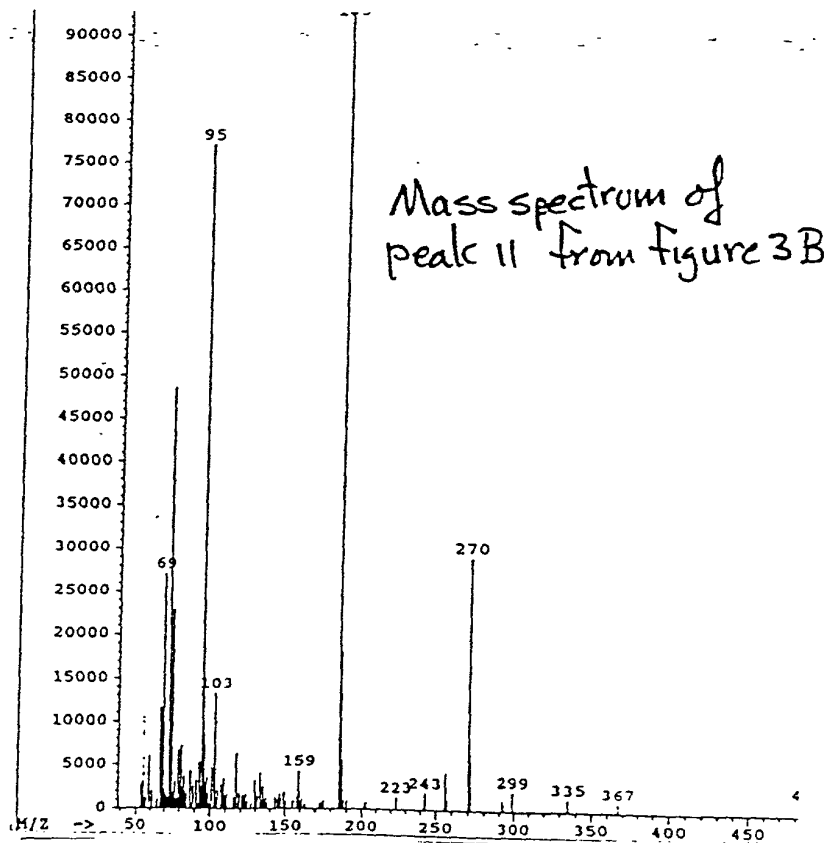
Figure 3

Figure
4A.

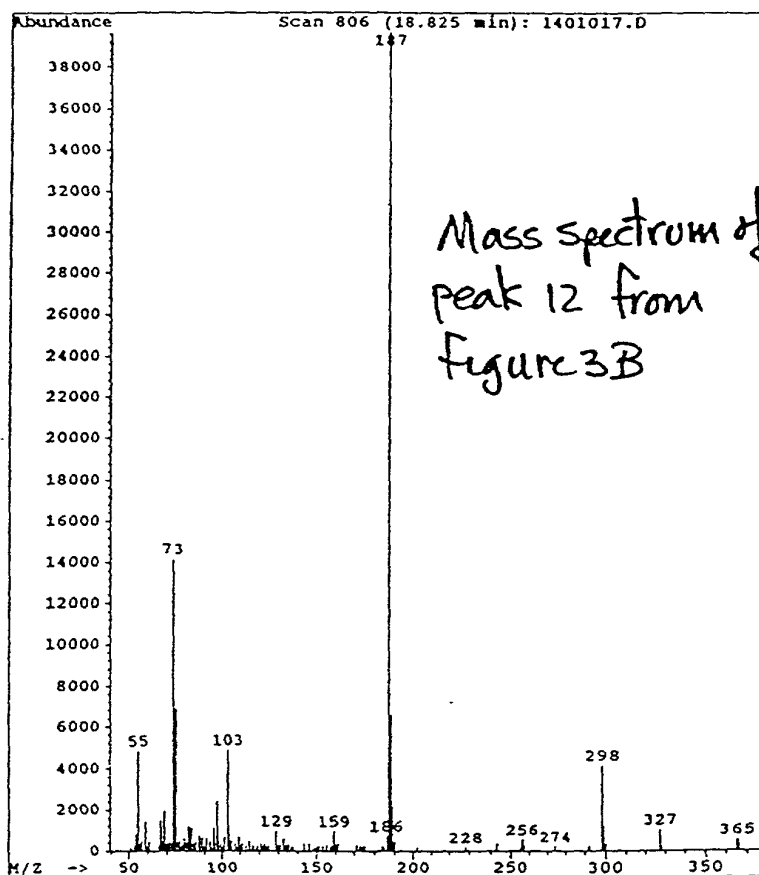
Mass Spectrum of peak 10 from Figure 3B



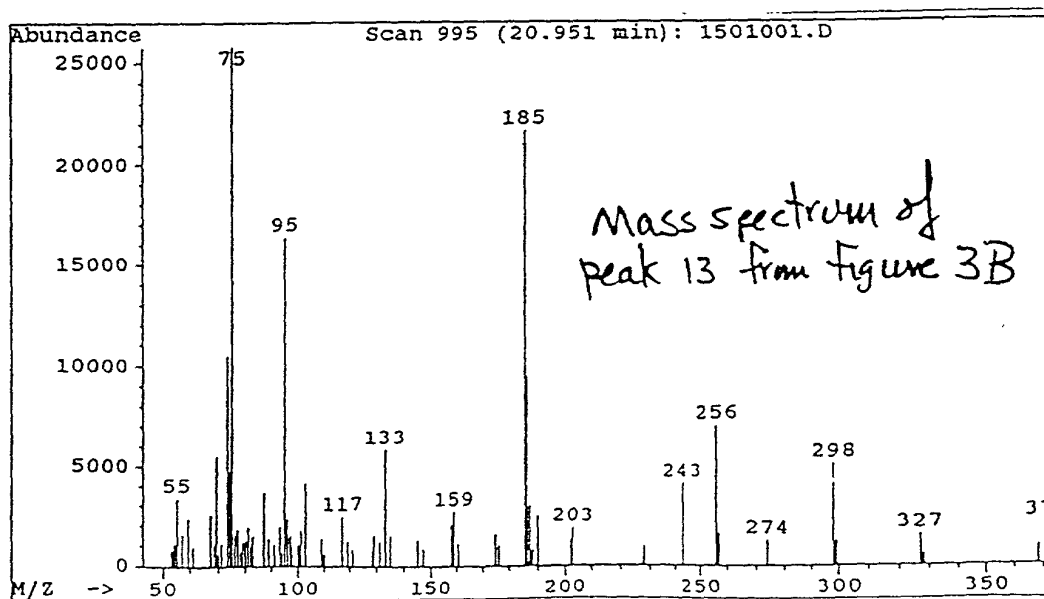
4B



4C



4D



10	20	30	40	50	60
TATTGGCACC	GGCGGCACCA	TTCCAACAAT	GGATCCCTAG	AAAAAGATGA	AGTCTTTGTC
70	80	90	100	110	120
CCACCTAAGA	AAGCTGCAGT	CANATGGTAT	GTCAAATACC	TCAACAACCC	TCTTGGACGC
130	140	150	160	170	180
ATTCTGGTGT	TAACAGTTCA	GTTTATCCTC	GGGTGGCCTT	TGTATCTAGC	CTTTAATGTA
190	200	210	220	230	240
TCAGGTAGAC	CTTATGATGG	TTTCGCTTCA	CATTTCTTCC	CTCATGCACC	TATCTTTAAG
250	260	270	280	290	300
GACCGTGAAC	GTCTCCAGAT	ATACATCTCA	GATGCTGGTA	TTCTAGCTGT	CTGTTATGGT
310	320	330	340	350	360
CTTTACCGTT	ACGCTGCTTC	ACAAGGATTG	ACTGCTATGA	TCTGCGTCTA	CGGAGTACCG
370	380	390	400	410	420
CTTTTGATAG	TGAACTTTTT	CCTTGTCTTG	GTCACCTTCT	TGCAGCACAC	TCATCCTTCA
430	440	450	460	470	480
TTACCTCACT	ATGATTCAAC	CGAGTGGGAA	TGGATTAGAG	GAGCTTTGGT	TACGGTAGAC
490	500	510	520	530	540
AGAGACTATG	GAATCTTGAA	CAAGGTGTTT	CACAACATAA	CAGACACCCA	CGTAGCACAC
550					
CAC					

Figure 5 Nucleotide sequence of pLesq2

10	20	30	40	50	60
TATAGGCACC	GGAGGCACCA	TTCCAACACA	GGATCCCTCG	AAAGAGATGA	AGTATTTGTC
70	80	90	100	110	120
CCAAAGCAGA	AATCCGCAAT	CAAGTGGTAC	GGCGAATACC	TCAACAACCC	TCCTGGTCGC
130	140	150	160	170	180
ATCATGATGT	TAAGTGTCCA	GTTCGTCTCT	GGATGGCCCT	TGTACTTAGC	CTTCAACGTT
190	200	210	220	230	240
TCTGGCAGAC	CCTACAATGG	TTTCGCTTCC	CATTTCTTCC	CCAATGCTCC	TATCTACAAC
250	260	270	280	290	300
GACCGTGAAC	GCCTCCAGAT	TTACATCTCT	GATGCTGGTA	TTCTAGCCGT	CTGTTATGGT
310	320	330	340	350	360
CTTTACCGTT	ACGCTGTTGC	ACAAGGACTA	GCCTCAATGA	TCTGTCTAAA	CGGAGTTCCG
370	380	390	400	410	420
CTTCTGATAG	TTAACTTTTT	CCTCGTCTTG	ATCACTTACT	TACAACACAC	TCACCCTGCG
430	440	450	460	470	480
TTGCCTCACT	ATGATTCATC	AGAGTGGGAT	TGGCTTAGAG	GAGCTTTAGC	TACTGTAGAC
490	500	510	520	530	540
AGAGACTATG	GAATCTTGAA	CAAGGTGTTC	CATAACATCA	CAGACACCCA	CGTCGCACAC
550					
CACT					

TTCTAGCCGT

Figure 6 Nucleotide sequence of pLesq3

S L

S L

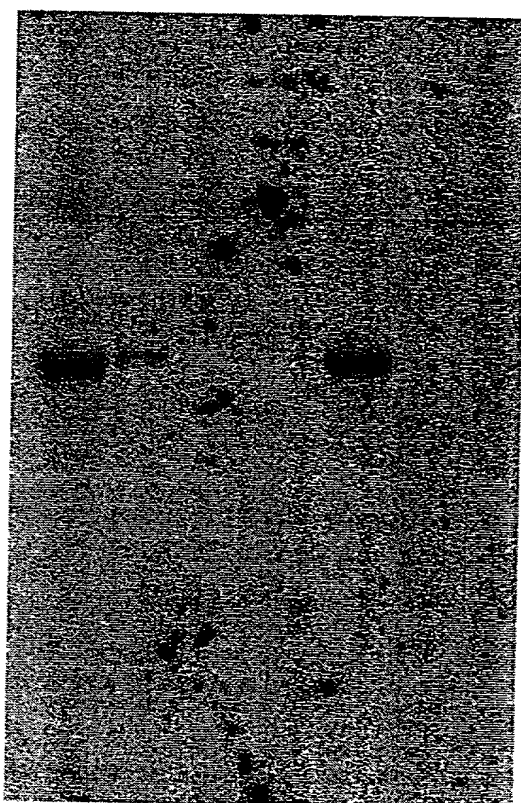


Figure 7

AT	GAA	GCT	TTA	TAA	GAA	GTT	AGT	TTT	CTC	TGG	TGA	CAG	AGA	AAT	TNT	47
GTC	AAT	TGG	TAG	TGA	CAG	TTG	AAG	CAA	CAG	GAA	CAA	CAA	GGA	TGG	TTG	95
GTG	NTG	ATG	CTG	ATG	TGG	TGA	TGT	GTT	ATT	CAT	CAA	ATA	CTA	AAT	ACT	143
ACA	TTA	CTT	GTT	GCT	GCC	TAC	TTC	TCC	TAT	TTC	CTC	CGC	CAC	CCA	TTT	191
TGG	ACC	CAC	GAN	CCT	TCC	ATT	TAA	ACC	CTC	TCT	CGT	GCT	ATT	CAC	CAG	239
AAG	AGA	AGC	CAA	GAG	AGA	GAG	AGA	GAG	AAT	GTT	CTG	AGG	ATC	ATT	GTC	287
TTC	TTC	ATC	GTT	ATT	AAC	GTA	AGT	TTT	TTT	TGA	CCA	CTC	ATA	TCT	AAA	335
ATC	TAG	TAC	ATG	CAA	TAG	ATT	AAT	GAC	TGT	TCC	TTC	TTT	TGA	TAT	TTT	383
CAG	CTT	CTT	GAA	TTC	AAG	Met ATG	Gly GGT	Ala GCT	Gly GGT	Gly GGA	Arg AGA	Ile ATA	Met ATG	Val GTT	Thr ACC	10 431
Pro CCC	Ser TCT	Ser TCC	Lys AAG	Lys AAA	Ser TCA	Glu GAA	Thr ACT	Glu GAA	Ala GCC	Leu CTA	Lys AAA	Arg CGT	Gly GGA	Pro CCA	Cys TGT	26 479
Glu GAG	Lys AAA	Pro CCA	Pro CCA	Phe TTC	Thr ACT	Val GTT	Lys AAA	Asp GAT	Leu CTG	Lys AAG	Lys AAA	Ala GCA	Ile ATC	Pro CCA	Gln CAG	42 527
His CAT	Cys TGT	Phe TTC	Lys AAG	Arg CGC	Ser TCT	Ile ATC	Pro CCT	Arg CGT	Ser TCT	Phe TTC	Ser TCC	Tyr TAC	Leu CTT	Leu CTC	Thr ACA	58 575
Asp GAT	Ile ATC	Thr ACT	Leu TTA	Val GTT	Ser TCT	Cys TGC	Phe TTC	Tyr TAC	Tyr TAC	Val GTT	Ala GCC	Thr ACA	Asn AAT	Tyr TAC	Phe TTC	74 623
Ser TCT	Leu CTT	Leu CTT	Pro CCT	Gln CAG	Pro CCT	Leu CTC	Ser TCT	Thr ACT	Tyr TAC	Leu CTA	Ala GCT	Trp TGG	Pro CCT	Leu CTC	Tyr TAT	90 671
Trp TGG	Val GTA	Cys TGT	Gln CAA	Gly GGC	Cys TGT	Val GTC	Leu TTA	Thr ACC	Gly GGT	Ile ATC	Trp TGG	Val GTC	Ile ATT	Gly GGC	His CAT	106 719
Glu GAA	Cys TGT	Gly GGT	His CAC	His CAT	Ala GCA	Phe TTC	Ser AGT	Asp GAC	Tyr TAT	Gln CAA	Trp TGG	Val GTA	Asp GAT	Asp GAC	Thr ACT	122 767
Val GTT	Gly GGT	Phe TTT	Ile ATC	Phe TTC	His CAT	Ser TCC	Phe TTC	Leu CTT	Leu CTC	Val GTC	Pro CCT	Tyr TAC	Phe TTC	Ser TCC	Trp TGG	138 815
Lys AAA	Tyr TAC	Ser AGT	His CAT	Arg CGT	Arg CGT	His CAC	His CAT	Ser TCC	Asn AAC	Asn AAT	Gly GGA	Ser TCT	Leu CTC	Glu GAG	Lys AAA	154 863
Asp GAT	Glu GAA	Val GTC	Phe TTT	Val GTC	Pro CCA	Pro CCG	Lys AAG	Lys AAA	Ala GCT	Ala GCA	Val GTC	Lys AAA	Trp TGG	Tyr TAT	Val GTT	170 911
Lys AAA	Tyr TAC	Leu CTC	Asn AAC	Asn AAC	Pro CCT	Leu CTT	Gly GGA	Arg CGC	Ile ATT	Leu CTG	Val GTG	Leu TTA	Thr ACA	Val GTT	Gln CAG	186 959

Figure 8A

Phe	Ile	Leu	Gly	Trp	Pro	Leu	Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	202
TTT	ATC	CTC	GGG	TGG	CCT	TTG	TAT	CTA	GCC	TTT	AAT	GTA	TCA	GGT	AGA	1007
Pro	Tyr	Asp	Gly	Phe	Ala	Ser	His	Phe	Phe	Pro	His	Ala	Pro	Ile	Phe	218
CCT	TAT	GAT	GGT	TTC	GCT	TCA	CAT	TTC	TTC	CCT	CAT	GCA	CCT	ATC	TTT	1055
Lys	Asp	Arg	Glu	Arg	Leu	Gln	Ile	Tyr	Ile	Ser	Asp	Ala	Gly	Ile	Leu	234
AAA	GAC	CGA	GAA	CGC	CTC	CAG	ATA	TAC	ATC	TCA	GAT	GCT	GGT	ATT	CTA	1103
Ala	Val	Cys	Tyr	Gly	Leu	Tyr	Arg	Tyr	Ala	Ala	Ser	Gln	Gly	Leu	Thr	250
GCT	GTC	TGT	TAT	GGT	CTT	TAC	CGT	TAC	GCT	GCT	TCA	CAA	GGA	TTG	ACT	1151
Ala	Met	Ile	Cys	Val	Tyr	Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Phe	Phe	266
GCT	ATG	ATC	TGC	GTC	TAT	GGA	GTA	CCG	CTT	TTG	ATA	GTG	AAC	TTT	TTC	1199
Leu	Val	Leu	Val	Thr	Phe	Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	282
CTT	GTC	TTG	GTA	ACT	TTC	TTG	CAG	CAC	ACT	CAT	CCT	TCG	TTA	CCT	CAT	1247
Tyr	Asp	Ser	Thr	Glu	Trp	Glu	Trp	Ile	Arg	Gly	Ala	Leu	Val	Thr	Val	298
TAT	GAT	TCA	ACC	GAG	TGG	GAA	TGG	ATT	AGA	GGA	GCT	TTG	GTT	ACG	GTA	1295
Asp	Arg	Asp	Tyr	Gly	Ile	Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	314
GAC	AGA	GAC	TAT	GGA	ATA	TTG	AAC	AAG	GTG	TTC	CAT	AAC	ATA	ACA	GAC	1343
Thr	His	Val	Ala	His	His	Leu	Phe	Ala	Thr	Ile	Pro	His	Tyr	Asn	Ala	330
ACA	CAT	GTG	GCT	CAT	CAT	CTC	TTT	GCA	ACT	ATA	CCG	CAT	TAT	AAC	GCA	1391
Met	Glu	Ala	Thr	Glu	Ala	Ile	Lys	Pro	Ile	Leu	Gly	Asp	Tyr	Tyr	His	346
ATG	GAA	GCT	ACA	GAG	GCG	ATA	AAG	CCA	ATA	CTT	GGT	GAT	TAC	TAC	CAC	1439
Phe	Asp	Gly	Thr	Pro	Trp	Tyr	Val	Ala	Met	Tyr	Arg	Glu	Ala	Lys	Glu	362
TTC	GAT	GGA	ACA	CCG	TGG	TAT	GTG	GCC	ATG	TAT	AGG	GAA	GCA	AAG	GAG	1487
Cys	Leu	Tyr	Val	Glu	Pro	Asp	Thr	Glu	Arg	Gly	Lys	Lys	Gly	Val	Tyr	378
TGT	CTC	TAT	GTA	GAA	CCG	GAT	ACG	GAA	CGT	GGG	AAG	AAA	GGT	GTC	TAC	1535
Tyr	Tyr	Asn	Asn	Lys	Leu											384
TAT	TAC	AAC	AAT	AAG	TTA	TGA	GGC	TGA	TAG	GGC	GAG	AGA	AGT	GCA	ATT	1583
ATC	AAT	CTT	CAT	TTC	CAT	GTT	TTA	GGT	GTC	TTG	TTT	AAG	AAG	CTA	TGC	1631
TTT	GTT	TCA	ATA	ATC	TCA	GAG	TCC	ATN	TAG	TTG	TGT	TCT	GGT	GCA	TTT	1679
TGC	CTA	GTT	ATG	TGG	TGT	CGG	AAG	TTA	GTG	TTC	AAA	CTG	CTT	CCT	GCT	1727
GTG	CTG	CCC	AGT	GAA	GAA	CAA	GTT	TAC	GTG	TTT	AAA	ATA	CTC	GGA	ACG	1775
AAT	TGA	CCA	CAA	NAT	ATC	CAA	AAC	CGG	CTA	TCC	GAA	TTC	CAT	ATC	CGA	1823
AAA	CCG	GAT	ATC	CAA	ATT	TCC	AGA	GTA	CTT	AG						1855

Figure 8B

	10	20	30	40	50	
LFFAH12.AMI	1	MGAGGRIM-- --VTPSSKKS	--ETEALKRG	PCEKPPFTVK	DLKKAIPQHC	50
FAH12.AMI	1	MGGGGRMSTV	ITSNNSEKKG	--GSSHLKRA	PHTKPPFTLG	50
ATFAD2.AMI	1	MGAGGRMP-- --VPTSSKKS	--ETDITKRV	PCEKPPFSVG	DLKKAIPPHC	50
BNFAD2.AMI	1	MGAGGRMQ-- --VSPSSKKS	--ETDNIKRV	PCETPPFTVG	ELKKAIPPHC	50
GMFAD2-1.AMI	1	MGLA-KETTM	GGRGRVAKVE	VQGGKPLSRV	PNTKPPFTVG	50
GMFAD2-2.AMI	1	MGAGGR----	TDVPPANRKS	--EVDPLKRV	PFEKPQFSL	50
ZMFAD2.AMI	1	MGAGGRMTEK	EREKQEQLAR	ATGGAAMQRS	PVEKPPFTLG	50
RCFAD2.AMI	1	-----	-----	-----	-----	50
	60	70	80	90	100	
LFFAH12.AMI	51	FKRSIPRSFS	YLLTDITVS	CFYYVATNYF	SLLPQPLSTY	100
FAH12.AMI	51	FERSFVRSFS	YVAYDVCLSF	LFYSIATNFF	PYISSPLS-Y	100
ATFAD2.AMI	51	FKRSIPRSFS	YLISDIIIAS	CFYYVATNYF	SLLPQPLS-Y	100
BNFAD2.AMI	51	FKRSIPRSFS	HLIWDIIIAS	CFYYVATTYF	PLLPNPLS-Y	100
GMFAD2-1.AMI	51	FQSRLLTSFS	YVVYDLSEAF	IFY-IATTYF	HLLPQPFS-L	100
GMFAD2-2.AMI	51	FQSRVLRFS	YVVYDLTIAF	CLYYVATHYF	HLLPGPLS-F	100
ZMFAD2.AMI	51	FERSVLKSFS	YVVHDLVIAA	ALLYFALAI	PALPSPLR-Y	100
RCFAD2.AMI	51	-----	-----	-----	-----	100
	110	120	130	140	150	
LFFAH12.AMI	101	GCVLTGIWVI	AHECGHHAFS	DYQWDDTVG	FIFHSFLLVP	150
FAH12.AMI	101	GCILTGLWVI	AHECGHHAFS	EYQLADDIVG	LIVHSALLVP	150
ATFAD2.AMI	101	GCVLTGIWVI	AHECGHHAFS	DYQWLDDTVG	LIFHSFLLVP	150
BNFAD2.AMI	101	GCVLTGVWVI	AHECGHAAFS	DYQWLDDTVG	LIFHSFLLVP	150
GMFAD2-1.AMI	101	GCLLTGVWVI	AHECGHHAFS	KYQWDDVVG	LTLSHSTLLVP	150
GMFAD2-2.AMI	101	GCILTGVWVI	AHECGHHAFS	DYQLDDDIVG	LILHSALLVP	150
ZMFAD2.AMI	101	G-----	-----AFS	DYSLDDVVG	LVLHSSLMVP	150
RCFAD2.AMI	101	-----WVM	AHDCGHHAFS	DYQLDDVVG	LILHSCLLVP	150
	160	170	180	190	200	
LFFAH12.AMI	151	HHSNIGSLEK	DEVFVPPKKA	AVKWYVKYL-	NNPLGRILVL	200
FAH12.AMI	151	HHSNIGSLER	DEVFVPPKKS	KISWYSKYS-	NNPPGRVLT	200
ATFAD2.AMI	151	HHSNIGSLER	DEVFVPPKKS	AIKWYVKYL-	NNPLGRIMML	200
BNFAD2.AMI	151	HHSNIGSLER	DEVFVPPKKS	QTSSGTAST-	STTFGRVMTL	200
GMFAD2-1.AMI	151	HHSNIGSLDR	DEVFVPPKKS	KVAFWSKYL-	NNPLGRAVSL	200
GMFAD2-2.AMI	151	HHSNIGSLER	DEVFVPPKKS	CIKWYSKYL-	NNPPGRVLT	200
ZMFAD2.AMI	151	HHSNIGSLER	DEVFVPPKKE	ALPWYTPYVY	NNPVGRVVHI	200
RCFAD2.AMI	151	HHSNIGSLER	DEVFVPPKKS	SIRWYSKYL-	NNPPGRIMTI	200
	210	220	230	240	250	
LFFAH12.AMI	201	YLAFNVSGRP	YDG-FASHFF	PHAPIFKDRE	RLQIYISDAG	250
FAH12.AMI	201	YLAFNVSGRP	YDR-FACHYD	PYGPIFSERE	RLQIYIADLG	250
ATFAD2.AMI	201	YLAFNVSGRP	YDG-FACHFF	PNAPIYNDRE	RLQIYISDAG	250
BNFAD2.AMI	201	YLAFNVSGRP	YDGGFACHFH	PNAPIYNDRE	RLQIYISDAG	250
GMFAD2-1.AMI	201	YLAFNVSGRP	YDS-FASHYH	PYAPIYSNRE	RLLIYVSDVA	250
GMFAD2-2.AMI	201	YLALNVSGRP	YDR-FACHYD	PYGPIYSNRE	RLQIYISDAG	250
ZMFAD2.AMI	201	YLATNASGRP	YPR-FACHFD	PYGPIYNDRE	RAQIFVSDAG	250
RCFAD2.AMI	201	YLAFNVSGRP	YDR-FACHYD	PYGPIYNDRE	RIEIFISDAG	250
	260	270	280	290	300	
LFFAH12.AMI	251	YAASQGLTAM	ICVYGVPLLI	VNFFLVLTFT	LQHTHPSLPH	300
FAH12.AMI	251	ATMAKGLAWV	MRIYGVPLLI	VNCFLVMITY	LQHTHPAIPR	300
ATFAD2.AMI	251	YAAAQGMASM	ICLYGVPLLI	VNAFLVLITY	LQHTHPSLPH	300
BNFAD2.AMI	251	YAAVQGVASM	VCFLRVPLLI	VNGFLVLITY	LQHTHPSLPH	300
GMFAD2-1.AMI	251	VATLKGLVWL	LCVYGVPLLI	VNGFLVTITY	LQHTHFALPH	300
GMFAD2-2.AMI	251	LAMAKGLAWV	VCVYGVPLLV	VNGFLVLITY	LQHTHPALPH	300
ZMFAD2.AMI	251	LAAAFGVWVW	VRVYAVPLLI	VNAWLVLITY	LQHTHPSLPH	300

Figure 9A

RCFAD2.AMI	251	LATAKGLAWV	VCVYGVPLLV	VNSFLVLITF	LQHTHPALPH	YDSSEWDWLR	300
		310	320	330	340	350	
LFFAH12.AMI	301	GALVTVDRDY	GILNKVFHNI	TDTHVAHHLF	ATIPHYNAME	ATEAIKPILG	350
FAH12.AMI	301	GAMVTVDRDY	GVLNKVFHNI	ADTHVAHHLF	ATVPHYHAME	ATKAIKPIMG	350
D2.AMI	301	GALATVDRDY	GILNKVFHNI	TDTHVAHHLF	STMPHYNAME	ATKAIKPILG	350
BNFAD2.AMI	301	GALATVDRDY	GILNQGFHNI	TDTHEAHHLF	STMPHYHAME	ATKAIKPILG	350
GMFAD2-1.AMI	301	GALATMDRDY	GILNKVFHHI	TDTHVAHHLF	STMPHYHAME	ATNAIKPILG	350
GMFAD2-2.AMI	301	GALATVDRDY	GILNKVFHNI	TDTHVAHHLF	STMPHYHAME	ATKAIKPILG	350
ZMFAD2.AMI	301	GALATMDRDY	GILNRVFHNI	TDTHVAHHLF	STMPHYHAME	ATKAIRPILG	350
RCFAD2.AMI	301	GALATVDRDY	GILNKVFHNI	TDQVAHHLF	-TMP-----	-----	350
		360	370	380	390	400	
LFFAH12.AMI	351	DYYHFDGTPW	YVAMYREAKE	CLYVEPDTER	GKKGVYYYNN	K-L.....	400
FAH12.AMI	351	EYYRYDGTFF	YKALWREAKE	CLFVEPDEGA	PTQGVFWYRN	KY-.....	400
ATFAD2.AMI	351	DYYQFDGTPW	YVAMYREAKE	CIYVEPDREG	DKKGVWYNN	K-L.....	400
BNFAD2.AMI	351	EYYQFDGTPV	VKAMWREAKE	CIYVEPDREG	EKKGVFWYNN	KL*.....	400
GMFAD2-1.AMI	351	EYYQFDDTFF	YKALWREARE	CLYVEPDEGT	SEKGVWYRN	KY-.....	400
GMFAD2-2.AMI	351	EYYRFDETFF	VKAMWREARE	CIYVEPDQST	ESKGVFWYNN	KL-.....	400
ZMFAD2.AMI	351	DYYHFDPTPV	AKATWREAGE	CIYVEPE---	DRKGVFWYNK	KF*.....	400
RCFAD2.AMI	351	-----	-----	-----	-----	-----	400
		410	420	430	440	450	
LFFAH12.AMI	401	450
FAH12.AMI	401	450
ATFAD2.AMI	401	450
BNFAD2.AMI	401	450
GMFAD2-1.AMI	401	450
GMFAD2-2.AMI	401	450
ZMFAD2.AMI	401	450

Figure 9B

0909188-06494

Molecular weight markers



E H X

3.6 -

1.8 -

1.5 -

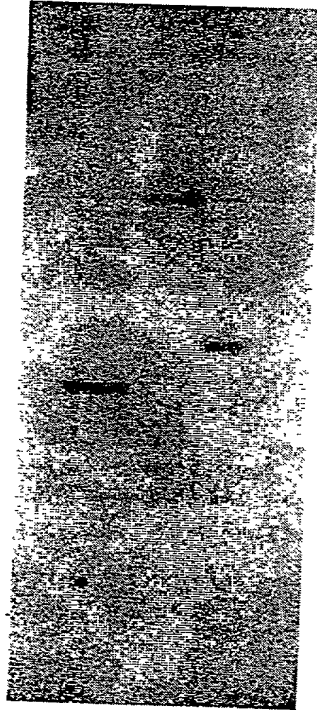


Figure 10

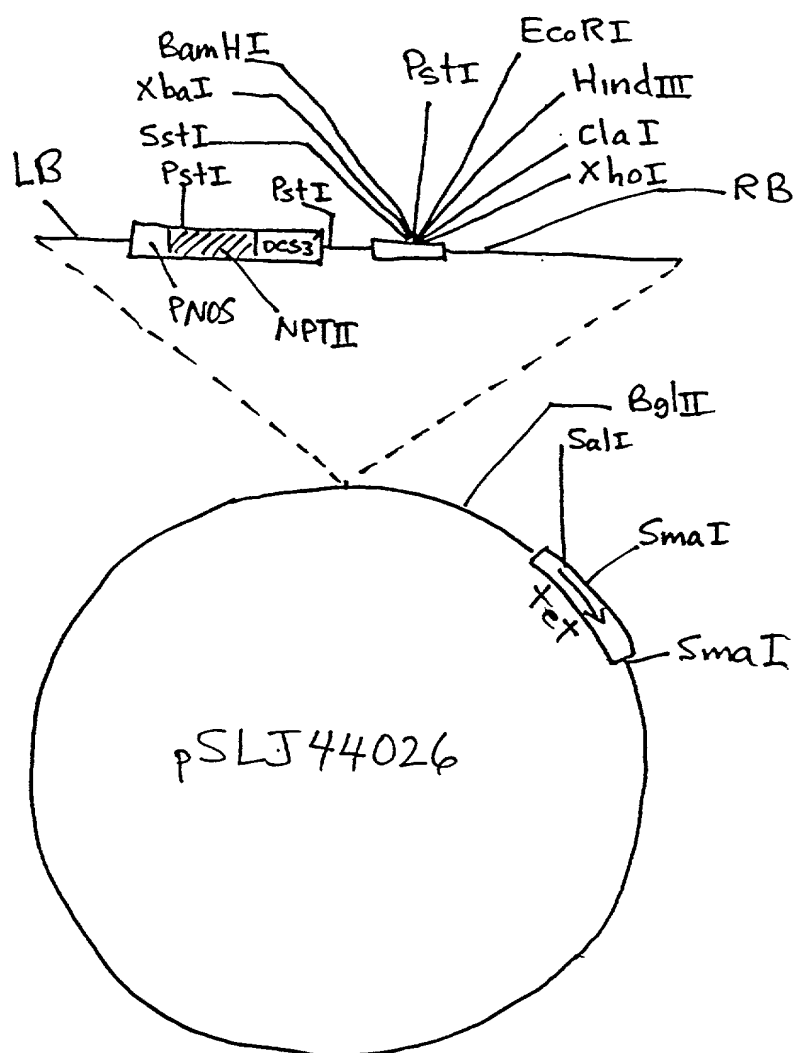
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Figure 11